RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/987,967

DATE: 11/21/2001
TIME: 10:25:14

ENTERED

Input Set : **A:\PF268D1C1SEQLIST.txt**
Output Set: **N:\CRF3\11212001\I987967.raw**

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      3 <110> APPLICANT: Wei et al.
      5 <120> TITLE OF INVENTION: Human Hematopoietic - Specific Protein
      7 <130> FILE REFERENCE: PF268D1C1
C-->  9 <140> CURRENT APPLICATION NUMBER: US/09/987,967
C-->  9 <141> CURRENT FILING DATE: 2001-11-16
      9 <150> PRIOR APPLICATION NUMBER: PCT/US96/04930
     10 <151> PRIOR FILING DATE: 1996-04-11
     12 <150> PRIOR APPLICATION NUMBER: 08/837,029
     13 <151> PRIOR FILING DATE: 1997-04-11
     15 <150> PRIOR APPLICATION NUMBER: 09/265,977
     16 <151> PRIOR FILING DATE: 1999-03-11
     18 <160> NUMBER OF SEQ ID NOS: 8
     20 <170> SOFTWARE: PatentIn version 3.1
     22 <210> SEQ ID NO: 1
     23 <211> LENGTH: 833
     24 <212> TYPE: DNA
     25 <213> ORGANISM: human
     27 <220> FEATURE:
     28 <221> NAME/KEY: CDS
     29 <222> LOCATION: (42)..(608)
     30 <223> OTHER INFORMATION:
     32 <220> FEATURE:
     33 <221> NAME/KEY: sig_peptide
     34 <222> LOCATION: (42)..(107)
     35 <223> OTHER INFORMATION:
     37 <220> FEATURE:
     38 <221> NAME/KEY: mat_peptide
     39 <222> LOCATION: (108)..()
     40 <223> OTHER INFORMATION:
     43 <400> SEQUENCE: 1
     44 ctcaaccaca gactacactt gctgaactgg ctcctggggc c atg agg ctg tca ctg      56
     45                                               Met Arg Leu Ser Leu
     46                                                   -20
     48 cca ctg ctg ctg ctg ctg ctg gga gcc tgg gcc atc cca ggg ggc ctc     104
     49 Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala Ile Pro Gly Gly Leu
     50         -15                 -10                 -5
     52 ggg gac agg gcg cca ctc aca gcc aca gcc cca caa ctg gat gat gag     152
     53 Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro Gln Leu Asp Asp Glu
     54 -1  1             5                   10                  15
     56 gag atg tac tca gcc cac atg ccc gct cac ctg cgc tgt gat gcc tgc     200
     57 Glu Met Tyr Ser Ala His Met Pro Ala His Leu Arg Cys Asp Ala Cys
     58             20                  25                  30
     60 aga gct gtg gct tac cag atg tgg caa aat ctg gca aag gca gag acc     248
     61 Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu Ala Lys Ala Glu Thr
     62             35                  40                  45
     64 aaa ctt cat acc tca aac tct ggg ggg cgg cgg gaa ctg agc gag ttg     296
     65 Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg Glu Leu Ser Glu Leu
```

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66        50                    55                  60
68 gtc tac acg gat gtc ctg gac cgg aac tgc tcc cgg aac tgg cag gac    344
69 Val Tyr Thr Asp Val Leu Asp Arg Asn Cys Ser Arg Asn Trp Gln Asp
70    65                   70                  75
72 tac gga gtt cga gaa gtg gac caa gtg aaa cgt ctc aca ggc cca gga    392
73 Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg Leu Thr Gly Pro Gly
74 80                   85                  90                  95
76 ctt agc gag ggg cca gag cca agc atc agc gtg atg gtc aca ggg ggc    440
77 Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val Met Val Thr Gly Gly
78              100                  105                 110
80 ccc tgg cct acc agg ctc tcc agg aca tgt ttg cac tac ttg ggg gag    488
81 Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu His Tyr Leu Gly Glu
82         115                  120                 125
84 ttt gga gaa gac cag atc tat gaa gcc cac caa caa ggc cga ggg gct    536
85 Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln Gln Gly Arg Gly Ala
86         130                  135                 140
88 ctg gag gca ttg cta tgt ggg gga ccc cag ggg gcc tgc tca gag aag    584
89 Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly Ala Cys Ser Glu Lys
90    145                  150                 155
92 gtg tca gcc aca aga gaa gag ctc tagtcctgga ctctaccctc ctctgaaaga   638
93 Val Ser Ala Thr Arg Glu Glu Leu
94 160                   165
96 agctggggct tgctctgacg gtctccactc ccgtctgcag gcagccagga gggcaggaag   698
98 cccttgctct gtgctgccat cctgcctccc tcctccagcc tcagggcact cgggcctggg   758
100 tgggagtcaa cgccttcccc tctggactca aataaaccc agtgacctca aaaaaaaaa     818
102 aaaaaaaaaa aaaaa                                                    833
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105 <210> SEQ ID NO: 2
106 <211> LENGTH: 189
107 <212> TYPE: PRT
108 <213> ORGANISM: human
110 <400> SEQUENCE: 2

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112 Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala
113         -20                  -15                 -10
116 Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro
117     -5                   -1  1                5                   10
120 Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu
121              15                  20                  25
124 Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu
125         30                   35                  40
128 Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg
129     45                   50                  55
132 Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Asn Cys Ser
133     60                   65                  70
136 Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
137 75                   80                  85                  90
140 Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val
141              95                  100                 105
144 Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu
145              110                  115                 120
```

```
148 His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln
149          125              130              135
152 Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly
153      140              145              150
156 Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu
157 155              160              165
160 <210> SEQ ID NO: 3
161 <211> LENGTH: 28
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <221> NAME/KEY: Primer_Bind
167 <223> OTHER INFORMATION: Synthetic primer containing a Bam HI restriction site
168        encoding a start AUG, followed by 19 nucleotides of the hHSP
169        coding sequence beginning with the first base of the 23rd codon.
171 <400> SEQUENCE: 3
172 cgcggatccg acagggcgcc actcacag                                28
175 <210> SEQ ID NO: 4
176 <211> LENGTH: 30
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <221> NAME/KEY: Primer_Bind
182 <223> OTHER INFORMATION: Synthetic primer containing an Xba I restriction site
183        followed by 21 nucleotides complementary to the last 21 nucleotides
184        of hHSP including the stop codon.
186 <400> SEQUENCE: 4
187 gcgtctagag aggtcactgg gttttatttg                              30
190 <210> SEQ ID NO: 5
191 <211> LENGTH: 34
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <221> NAME/KEY: Primer_Bind
197 <223> OTHER INFORMATION: Synthetic primer containing a Bam HI restriction site
198        followed by 19 bases of the sequence of hHSP.
200 <400> SEQUENCE: 5
201 cgcggatccg ccatcatgag gctgtcactg ccac                        34
204 <210> SEQ ID NO: 6
205 <211> LENGTH: 30
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <221> NAME/KEY: Primer_Bind
211 <223> OTHER INFORMATION: Synthetic primer containing an Xba I restriction site
212        followed by nucleotides complementary to the last 21 nucleotides of
213        hHSP including the stop codon.
215 <400> SEQUENCE: 6
216 gcgtctagag aggtcactgg gttttatttg                              30
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219 <210> SEQ ID NO: 7
220 <211> LENGTH: 34
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <221> NAME/KEY: Primer_Bind
226 <223> OTHER INFORMATION: Synthetic primer containing a Bam HI site, an AUG start
codon
227         and 16 nucleotides thereafter.
230 <400> SEQUENCE: 7
231 cgcccatccg ccatcatgag gctgtcactg ccac                         34
234 <210> SEQ ID NO: 8
235 <211> LENGTH: 57
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <221> NAME/KEY: Primer_Bind
241 <223> OTHER INFORMATION: Synthetic primer containing an Xba I site, a stop codon,
242         9 codons forming hemaglutinin tag and 18 bp of 3' coding sequence.
244 <400> SEQUENCE: 8
245 cgctctagat caagcgtagt ctgggacgtc gtatgggtag agctcttctt ctgtggc      57
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date